

Result No.	Score	Query Match	Length	DB	ID	Description
1	824	26.1	164	4	US-09-621-976-5565;	Sequence 5565, Ap
2	816	25.9	601	4	US-09-902-540-11184	Sequence 11184, A
3	783	24.8	336	4	US-09-270-767-44314	Sequence 44314, A
4	691.5	21.9	390	4	US-09-252-991A-26058	Sequence 26058, A
5	666	21.1	389	4	US-09-328-352-6380	Sequence 6380, Ap
6	650	20.6	384	4	US-09-648-004-6	Sequence 6, Appl
7	650	20.6	384	4	US-10-272-419-6	Sequence 6, Appl
8	623	19.8	387	4	US-09-328-352-6442	Sequence 6442, Ap
9	618.5	19.6	403	4	US-09-252-991A-27960	Sequence 27960, A
10	608	19.3	382	4	US-09-328-352-4850	Sequence 4850, Ap
11	604	19.2	432	4	US-09-949-016-6098	Sequence 6098, Ap
12	603.5	19.1	419	4	US-09-252-991A-31097	Sequence 31097, A
13	596	18.9	394	4	US-09-328-352-6801	Sequence 6801, Ap
14	595.5	18.9	409	3	US-09-364-230-30	Sequence 30, Appl
15	588.5	18.7	427	3	US-09-364-230-32	Sequence 32, Appl
16	588.5	18.7	459	4	US-09-949-016-10443	Sequence 10443, A
17	559.5	17.7	383	4	US-09-328-352-7081	Sequence 7081, Ap
18	546.5	17.3	421	4	US-09-949-016-5872	Sequence 5872, Ap
19	546.5	17.3	610	4	US-09-949-016-7708	Sequence 7708, Ap
20	538.5	17.1	331	4	US-09-902-540-15531	Sequence 15531, A
21	514.5	16.3	402	4	US-09-328-352-4281	Sequence 4281, Ap
22	501	15.9	424	4	US-09-252-991A-24653	Sequence 24653, A
23	495	15.7	399	4	US-09-328-352-4360	Sequence 4360, Ap
24	495	15.7	464	4	US-09-252-991A-33108	Sequence 33108, A
25	479	15.2	415	4	US-09-806-536A-13	Sequence 13, Appl
26	479	15.2	444	4	US-09-949-016-10163	Sequence 10163, A
27	472	15.0	382	4	US-09-252-991A-29144	Sequence 29144, A

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FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11184
LENGTH: 601
TYPE: PRT
ORGANISM: Myxococcus xanthus
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(601)
OTHER INFORMATION: unsure at all xaa locations
US-09-902-540-11184

Query Match      25.9%; Score 816; DB 4; Length 601;
Best Local Similarity 36.1%; Pred. No. 7.9e-74;
Matches 214; Conservative 92; Mismatches 197; Indels 90; Gaps 16;

QY 54 FPPEVSDQL-----NEINQFLGVEKFFTEV--DSRKID-QEGKIPDETLEKLS 103
Db 19 FLPEEVGSARILPTETFEORLFFKFTALQFSREQVLPISERIEAKDNALLRQLRQAGE 78
QY 104 LGLFGLQVPEYCGLGFSNTMYSLGELIISMDGSIITVTLAAHQAGLKGIIILAGTEEOKA 163
Db 79 LGLLSVDIPAYGGTGLDKTTSLLLAELSNGLSWSVTFGAHTGIGTLPFVFNAGTEOKA 138
-QY 164 KYLPKLAGSHIAAFICITEPASGSDAASIRATLSLSEDKKHYILNGSKVMTNGGLANIF 223
Db 139 KYLPKLAGTEWAAAYALTEQSGSDALGAKTKAVLSPDGKHWILNGSKLYITNAADFV 198
QY 224 TVFAKTEVDSGSKDKITAFIVERDPFGVTGKPEDKLGIRGNTCEVHFENTKIPVE 293
Db 199 VFPAKV-----DG---DKFTGFIVEKDTPLGTVGPEHKMGIRGSSSTCPLYFEDARVPVE 250
QY 284 NILGEVGDGFKVAMNINLSGRFMSGVVAGLLKRLIEMTAETACRQKFNKLSRSEGLIQ 343
Db 251 NQGEVKGKHIAFNILNYGRLLKGLGVLGMKLOQNALRFTQERKQFNAPIVQPLSR 310
QY 344 EKFPALMAQKAYVMESMTYLTAGML-----DQPGF-----PDCEIAAMVKVFS 386
Db 311 EKLARMAALVAVESMTYRTAGLVDAARLGQGDADPYEARLLAEVBEVAYESSIMKVHG 370
QY 387 SEAAQCVSEALQILGLGTRDYPYRIIRDTRILLIFEGTNEILRMVIALTGLQHAGR 446
Db 371 SESFGLVDDAVQLHGGAGYIEYPVRSYRDARINRIFEGTNEINRMLITGMMLKRAVR 430
QY 447 ILTTRIHELQO-AKVSTVMDTVGR-----RLRDSLGRTVDLGLTGNHGVVHPSPADSAN 499
Db 431 -----GDLPLFAMAGNVAELSRGERPRARVQDALAPQVAAEAAGKHALH-----476
QY 500 KFEENTYCFGRV--ETLLRFGKTIMEEQVLKRVANILINLYGMTAVLSRASRS-----553
Db 477 -----GLRVAET-----FGPELEHQEVLAAALSDVMVMDAPALDSMVTTRQATSG 523
QY 554 -----IRIGL-----RNHDE-EVLLANTFCVEAYLONLFLSLDLDKXAP 591
Db 524 ALDPVRVAMTQLYALDAIPRAYDTRRALCATLKGALDQELERGLTLDVFTTP 576

RESULT 3
US-09-270-767-44314
Sequence 44314, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 44314
LENGTH: 336
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-44314

Query Match      24.8%; Score 783; DB 4; Length 336;
Best Local Similarity 49.3%; Pred. No. 6.7e-71;
Matches 169; Conservative 54; Mismatches 104; Indels 16; Gaps 5;

QY 218 GLANITVFAKTEVD--SDGSVKDKITAFIVERDGGVTNGKPKDKLGRGNTCEVHFE 276
Db 3 GIAEIMTVFAQTEQVDPKTGEKKDKTAFIVERSGGVTNGPPEKKMGKASNTAEVYFE 62
QY 277 NTKIPVENILGREGVDFKVMNINLSGRFMSGVVAGLLKRLIEMTAETACRQKFNKEL 336
Db 63 DVKIPENVLGEGGDFKVMNINLSGRFMSGVVAGLLKRLIEMTAETACRQKFNKEL 122
QY 337 SBFGLIQEKFALMAQKAYVMESMTYLTAGMLDQPGFPPDCSIDAAMVKVFSSEAAQCVSE 396
Db 123 KNYGSIQEKLAQMNILOAYATESMAFTISQNMW-AGSKDVHLEAAISKIYASESAWTVCD 181
QY 397 ALQIILGGLGYTRDYPYRIIRDTRILLIFEGTNEILRMVIALTGLQHAGRILTRIHELK 456
Db 182 AIQILGGMGYMVDTLGERVLRDLRIFRIPEGTNDILRLFIALTGIQYAG-----SHLKEIQ 237
QY 457 Q-----AKVSTVMDTVGRRLDSLGRTVDLGLTGNHGVVHPSPADSANKFBENTYCFGR 510
Db 238 RAFKPSANLGLIFKEASR-----AASVGLGGLDLSGHVVGELLPYAKKTAHCIDLFQ 293
QY 511 TVETLLRFGKTIMEEQVLKRVANILINLYGMTAVLSRASRS 553
Db 294 SVEELLRYKNIVNEQILLTELAAIDIAMVWVVTQSRSSRA 336

RESULT 4
US-09-252-991A-26058
Sequence 26058, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26058
LENGTH: 390
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26058

Query Match      21.9%; Score 691.5; DB 4; Length 390;
Best Local Similarity 37.8%; Pred. No. 1.8e-61;
Matches 147; Conservative 82; Mismatches 121; Indels 39; Gaps 8;

QY 67 INQFLGVEKFFTEV--DSRKIDQEGKIPDETLEKLSLGLFGLQVPEYGGIGLPSNTM 124
Db 14 LNLLLDSIRQFVRESLVPHEQVAETDRIPAEIARIARMREMLGFLSLIPEAYGGLG-----68
QY 125 YSRIGEIIISMDGSIITV-----LAAHQAGLKGIIILAGTEEOKAKYLPKLS 171
Db 69 -----VTMEEVSVIAFEIGRTSPAPRSLGTNGNGISQGIIVIDGTEERKRVLPRLAS 121
QY 172 GEHIAAFCLTEPASGSDAASIRATLSLSEDKKHYILNGSKVMTNGGLANIFTVFAKTEV 231
Db 122 GELLSSFCLETPDPSGSDAASLKTTAV--RDGEHYVLNGTKRFTINAPQAGIYTVWART--177
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QY 232 VSDGSKDK--ITAFIVERDFGVNGKPEDKLGIRGNTCEVHPENTKIPVENILGEV 289
Db 178 ---DPAIRAGGISAFFVERGTGLSLGKPDKMGQGAHTCDVIFDCCRVPASQLIGV 234
QY 290 -GDGFKVAMNINSGRFSMGVAGLLKRLIEMTAETACRQKFNKRLSEFGLIOEKFAL 348
Db 235 EGVGFTAMKVLKGRHLHIAVCVGAERMLEDALYALERKQFGQPIAEFQIQLAMLAD 294
QY 349 MAQKAYMESMTYLTAGMLDQPGFPCSIIEAAMVKVPSSEAAWQCVSEALQILGLGYTR 408
Db 295 SKAEYAARCMWIDAARQDEG--RDVGTASCAKLFASEMCGRVADRAVOIFGGAGYIG 352
QY 409 DYPYERILDRILLIFEGTNEILRMVIA 437
Db 353 DYGIERYDRVRLFRLYEGTQIQOULLIA 381

RESULT 5

US-09-328-352-6380
; Sequence 6380, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: GAY L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6380
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6380

Query Match 21.1%; Score 666; DB 4; Length 389;
Best Local Similarity 38.8%; Pred. No. 7.3e-59;
Matches 150; Conservative 79; Mismatches 148; Indels 16; Gaps 8;
QY 58 EVSQDELNEINQFLGPVEKFFTEVDNR--KIDQEGKIPDETLEKLSLGLFGLQVPEEY 115
Db 5 QMRDE-GMLEQLLSITRDFVKNELIPRENEVEKXIPDDIVQQWRELGLFLGTIPEEY 63
QY 116 GGLGFNTMYSLG-EIISMDGSITVTLAAHQAIKGLIAGTEBQKAKYLPKLSASGEH 174
Db 64 GGLGITMEBEVRVAFELGQTSAPFRSLIGTNGIGSSAILIDGTBEQOKYLPYASGEI 123
QY 175 IAAFCLTEPASGSDAASIRSRATLSEDKKHYILNGSKVITNGGLANIITVFAKT--EVV 232
Db 124 IGSFCLTEPESGSDAASLKTSV--KDGDFYVLNGTKRFTTNAPHAAATFTWARTNPEIK 181
QY 233 DSDGSKDKITAFIVERDFGVNGKPEDKLGIRGNTCEVHPENTKIPVENILGEV-GD 291
Db 182 GSGG-----ISAEVZANTFGITLGIKIDQWKGQSGHTCDVIFENCVRVPASALIGVEGV 236
QY 292 GFKVAMNINSGRFSMGVAGLLKRLIEMTAETACRQKFNKRLSEFGLIOEKFALMAQ 351
Db 237 GFKTAMKVLKGRHLHIGAYSVGAERMLNDALNYAIERKQFGQPIANFQIQLAMLADSKA 296
QY 352 KAYMESMTYLTAGMLDQPGFPCSIIEAAMVKVPSSEAAWQCVSEALQILGLGYTRDYP 411
Db 297 EYIAAKCMWLDAARRDNG--ENISTEASCAKMFATEMCGRVADRCVQIHGGAGYISEYA 354
QY 412 YERILDRILLIFEGTNEILRMVIALTGLQHA 444
Db 355 IERFYDRVRLFRLYEGTQIQOULLIAKNMIREA 387;

RESULT 6

US-09-648-004-6
; Sequence 6, Application US/09648004
; Patent No. 6496242
; GENERAL INFORMATION:

; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; FILE REFERENCE: CL-1341-A
; CURRENT APPLICATION NUMBER: US/09/648,004
; CURRENT FILING DATE: 2000-04-25
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-09-648-004-6

Query Match 20.8%; Score 650; DB 4; Length 384;
Best Local Similarity 38.6%; Pred. No. 3.1e-57;
Matches 154; Conservative 77; Mismatches 132; Indels 36; Gaps 11;
QY 61 QDELNE---INQFLGPVEKFFTEVDNRKIDQEGKIPDETLEKLSLGLFGLQVPEEY 116
Db 5 QDTNLQVDMIRQFVGV-LIPNEE-----VAETDEIPAEIVQOMKELGFLGTIPEEY 59
QY 117 GLGFNTMYSLR---GEIISMDGSITVTLAAHQAIKGLIAGTEBQKAKYLPKLSASGE 173
Db 60 GLGL--TMEEVYIAFELGRTSPAPFRSLICTNNGIGSSGLIIDGSEQKQYFLPRLASGE 117
QY 174 HIAFCLTEPASGSDAASIRSRATLSEDKKHYILNGSKVITNGGLANIITVFAK--TEV 231
Db 118 IIGSFCLTEPDSGSDAASLKTTAV--KDGPHYILNGTKRYITNAPHAGVFTWARTSTEI 175
QY 232 VSDGSKDKITAFIVERDFGVNGKPEDKLGIRGNTCEVHPENTKIPVENILGEV-G 290
Db 176 KGTGG-----ISAFIVDSKTPGISLGRKDRKMGQGAHTCDVIFENCVRVPASALIGVEG 230
QY 291 DGFKVAMNINSGRFSMGVAGLLKRLIEMTAETACRQKFNKRLSEFGLIQ-----EK 345
Db 231 VGFKTAMKVLKGRHLHIAALSVAATRMLEDLSLOYAVERKQFGQATANFQIQLAMLADSK 290
QY 346 FALMAQKAYMESMTYLTAGMLDQPGFPCSIIEAAMVKVPSSEAAWQCVSEALQILGLGL 405
Db 291 AEIYAAKCMWLDAARLDAGQ-----NVSTEASCAKMFATEMCGRVADRCVQIHGGAG 343
QY 406 YTRDYPYERILDRILLIFEGTNEILRMVIALTGLQHA 444
Db 344 YISEVAIERFYDRVRLFRLYEGTQIQOULLIAARNMIREA 382

RESULT 7

US-10-272-419-6
; Sequence 6, Application US/10272419
; Patent No. 6794165
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; FILE REFERENCE: CL1341-A
; CURRENT APPLICATION NUMBER: US/10/272,419
; CURRENT FILING DATE: 2002-10-16
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-10-272-419-6

Query Match 20.6%; Score 650; DB 4; Length 384;
Best Local Similarity 38.6%; Pred. No. 3.1e-57;
Matches 154; Conservative 77; Mismatches 132; Indels 36; Gaps 11;

QY 61 QDELNE----INQPLGVEKFFTEVDNRKIDQKIPDETLEKLSLGLFGLQVPEEY 116
DB 5 QDTLNQLVDMIRQFVGV-LIPNEI-----VAETDEIPAIIVQMKELGFLGTLTIEEVE 59
QY 117 GLGFSNTWYRL---GHIISDGSITVTLAAHQIAGLKGIILAGTEQKAKYLPKLASGE 173
DB 60 GLGL--TMEEVVIAFELGRTSPAFRLSGLTNGNIGSSGLIIDGSEQKQYFLPRLASGE 117
QY 174 HIAAFCLTEPASGSDAASIRSRATLSDEKHYILNGSKWITNGGLANIPTVFAK--TEV 231
DB 118 IISGFCUTEPSDSDAASLKTAV--KGDHYILNGTKRYITNAPHAGVFTWARTSTEI 175
QY 232 VDSGSKDKITAFIVERDFGVNGKPEDKLGIRGNTCEVHFENTKIPVENILGEV-G 290
DB 176 KGTGG-----ISAFIVDSKTPGISLGRDKKMGKGAHTCDVIFENCRIIPASALIGVEG 230
QY 291 DGFVAMNINSGRFSMGVSVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIQ-----EK 345
DB 231 VGFKTAMKVLDKRIHIAALSVAATRLMLEDLSQYAVERKQFGQAIANFOLIQLMADSK 290
QY 346 FALMAOKAYVYMESMTYLTAGMLDQPGFPDCSIEAAMVKVFSSEAAQCSEALQILGGLG 405
DB 291 AEIYAAKCVLDARLDAQ-----NVSTASCAKMFATEMCGRVADRGVQIHGGAG 343
QY 406 YTRDYPYERILDRILLIPEGTNEILRMVIALTGLQHA 444
DB 344 YISEYAIERYDVRFLRYEGTQIQOQVIAARNMIREA 382

RESULT 8
US-09-328-352-6442
; Sequence 6442, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-03-31
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6442
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6442

Query Match 19.8%; Score 623; DB 4; Length 387;
Best Local Similarity 36.8%; Pred. No. 1.8e-54;
Matches 145; Conservative 79; Mismatches 130; Indels 40; Gaps 10;

QY 61 QDELNEINQPLGVEKFFTEEV---DSRKIDQSGKIPDETLEKLSLGLFGLQVPEEY 117
DB 9 QETLNQLVDMI-----RQFVECVLI PHENEVAETDEIPDIVEQMKALGFLGTLTIEEVE 64
QY 118 LGSNTWYRLGHIISDGSITV-----LAAHQIAGLKGIILAGTEQKAK 164
DB 65 LG-----LTMEEVYVAFELGRTSPAFRLSGLTNGNIGSSGLIIDGTEAKSF 112
QY 165 YLPKLASGEHIAAFCLTEPASGSDAASIRSRATLSDEKHYILNGSKWITNGGLANIPT 224
DB 113 FLPLARGEVISSFCUTEPSDSDAASLKTAV--KGDFFYVLNGTKRITNAPHAGVFT 170
QY 225 VFAKTEVDSGSKDKITAFIVERDFGVNGKPEDKLGIRGNTCEVHFENTKIPVEN 284
DB 171 VMARTN-FDIKGA--SGISAFIVDSQTPGISLGRDKKMGKQVHTCDVIFENCRIIPASA 227
QY 285 ILGEV-GDGFVKVAMNINSGRFSMGVSVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIQ 343

DB 228 LIGGVEGVGFKTAMKVLDRKRLHIAALSVAATRLMDDSLNIAERKQFGQPIAEFQLIQ 287
QY 344 EKFAALMAOKAYVYMESMTYLTAGMLDQPGFPDCSIEAAMVKVFSSEAAQCSEALQILGG 403
DB 288 AMLADSKAEIYAAKCV-LDAARLRDAG-QNVSTASCAKMFATEMCGRVADRCVQIHGG 345
QY 404 LGYTRDYPYERILDRILLIPEGTNEILRMVIA 437
DB 346 AGYISEYAIERYDVRFLRYEGTQIQOQVIA 379

RESULT 9
US-09-252-991A-27960
; Sequence 27960, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27960
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27960

Query Match 19.6%; Score 618.5; DB 4; Length 403;
Best Local Similarity 37.5%; Pred. No. 5.4e-54;
Matches 149; Conservative 71; Mismatches 148; Indels 29; Gaps 8;

QY 52 EYVFPPEVSQDELNEINQPLGVEKFFTEEVDSR--KIDQSGKIPDETLEKLSLGLFGL 109
DB 15 ESMYTPSLNFALGETIDMLRDQVRGFAELQPPRAAQIDQDNQFPMDMWRKFGEMGLLI 74
QY 110 QYPEEYGLGFSNTWYRLGELIIS-MDGSITVTLAAHQIAGLKGIILAGTEQKAKYLPK 168
DB 75 TVDEEYGSALCYLAHAVVMEISASASVALSYGAHNLVCVQIKRNGNAEQKARYLPA 134
QY 169 LASGEHIAAFCLTEPASGSDAASIRSRATLSDEKHYILNGSKWITNGGLANIPTVFAK 228
DB 135 LVSGEHIGALAMSEPNAGSDVVMKLRADRVGDR--FVLNGSKWITNGPDAHTVYIVAK 192
QY 229 TEVDSGSKDKK---ITAFIVERDFGVNGKPEDKLGIRGNTCEVHFENTKIPVEN 284
DB 193 TDA-----DKGAHGITAFIVERDWRGFSRGPGLKDLGMRGNTCELI FODVEVPEEN 244
QY 285 ILGEGVGDGFKVAMNINSGRFSMGVSVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOE 344
DB 245 VLGAANGGVKVLMSGLDYERVVLSGPGVIMQACNDVVVPYIHDRQFGQSIGEFQLVQG 304
QY 345 KF-----ALMAQKAYVYMESMTYLTAGMLDQPGFPDCSIEAAMVKVFSSEAAQCSEALQ 399
DB 305 KVADMYTALNASRAYL-----YAVAAACDRG--ETTRKDAAGVILYSERATQMALDAIQ 357
QY 400 ILGGYGYTRDYPYERILDRILLIPEGTNEILRMVY 436
DB 358 ILGGNGYINEFTGRLRLDRAKLYEIGAGTSEIRMLI 394

RESULT 10
US-09-328-352-4850
; Sequence 4850, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;; FILE REFERENCE: GTC99-03PA
;; CURRENT APPLICATION NUMBER: US/09/328,352
;; CURRENT FILING DATE: 1999-06-04
;; NUMBER OF SEQ ID NOS: 8252
;; SEQ ID NO 4850
;; LENGTH: 382
;; TYPE: PRT
;; ORGANISM: Acinetobacter baumannii
US-09-328-352-4850

Query Match 19.3%; Score 608; DB 4; Length 382;
Best Local Similarity 37.5%; Pred. No. 5.8e-53;
Matches 142; Conservative 71; Mismatches 154; Indels 12; Gaps 6;
QY 63 ELNEINQFLGPGVEKFTTEE---VDSRKIDQEGKIPDETLEKLSGLGLFGLQVPEEYGGGLG 119
DB 9 QTEEQLLIRDMAKSAQKIPNASDWDGDTFFPKETLTOMQGLGFMGLMSEEWGGSD 68
QY 120 FSNMTY-SRGEIISMDGSIITVTLAAHQAIGLKGIIILAGTEQKAKYLPKLASGEHIAAF 178
DB 69 TGNLAYVLAEEVAADGATSTIMSVHNSVGCVPILKPGTDEQKERFLKPLAQGEMIGAF 128
QY 179 CLTEPASGSDASIRSRTLSEDKKHYILNGSKVWITNGGLANIFTVPFAKTEVVDSDGV 238
DB 129 ALTEPTGSDAAAIKTRAV---KQDDYILNGAKQFITSNGNAGVITVFAVTD-----PSAG 182
QY 239 KDKITAFIVERDFGGVTKGPKEDKLGIRGNTCEVHFENTKIPVENILGEVGDGPKVAMN 298
DB 183 KGISAFVLPRTGPGVEIRVEKGLHSDTCQIALTVRIHKSMLMGEGEGLKIALA 242
QY 299 ILSGRFSMGVSVAGLLKELIEMTAETACTRKQFNKRLSEFGLIOBKFALMAQKAYMES 358
DB 243 NLEGGRIAGAAQAVGLARAALAEATRYAKERITTFGKPIFEHQTIAPRLASMAIEIAAQ 302
QY 359 MYLTRAGMDQGFPPDCSIEAMVKVFSSEAAWQCSEALQILGGLGYTRDYPYERILRD 418
DB 303 LVHY-AARLKEAGQP-CLNEASMAKLFASEMTERVCSSALQVFGGYGLRDPPIERYD 360
QY 419 TRILLIFEGTNEILRMVIA 437
DB 361 ALICQIYEGTSDIQLRVIA 379

RESULT 11
US-09-949-016-6098
; Sequence 6098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6098
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6098

Query Match 19.2%; Score 604; DB 4; Length 432;
Best Local Similarity 35.9%; Pred. No. 1.8e-52;
Matches 157; Conservative 81; Mismatches 155; Indels 44; Gaps 14;

QY 19 GLVSTANRRLLRTSPVPFAFAKEFLGKIKKKEVFP-PPEVSQDE--LINEINQ--FLGP 73
DB 3 GLAV-----RLLRGSRLLR-----RNFLTCLSSWKIPPHVSKSSQSEALLNITNGIHFAF 53
QY 74 VEKFFTEEVDVSRK-----IDQEGKIPDETLEKLSGLGLFGLQVPEEYGG 117
DB 54 LQTFDEEMMIKSSVKVFAQEQIAPLVSTMDENSKMEKSVIQLFOOGLMGIEVDPEYGG 113
QY 118 LG--FSNTMYSRLGEIISMDGSIITVTLAAHQAIGLKGIIILAGTEQKAKYLPKLASGEHI 175
DB 114 TGASFLSTLVV-IEELAKVDASVAVFCEIQNTLINTLRKHGTEQEKATYLPQLTT-EKV 171
QY 176 AAFCLTEPASGSDASIRSRTLSEDKKHYILNGSKVWITNGGLANIFTVPFAKTEVVDSD 235
DB 172 GSFCLEAGAGSDSFALKTRADKEG--YYVLNGSRWVSSAHEAGLFLVMANV-----D 224
QY 236 GSVKDK-ITAFIVERDFGGVTKGPKEDKLGIRGNTCEVHFENTKIPVENILGEVGDGPK 294
DB 225 PTIGYKITSFLVDRDTPGLHIGKPKENKLGRLASSTCPLTFENVKVPPEANILGQIGHYK 284
QY 295 VAMNIIINSGRFSMGVSVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOBKFALMAQKAY 354
DB 285 YAGISLNEGRIGIAAQMGLAQCGPDYTIPIYKERIQFGKRLDFDFOGLQHOVAHVATQLE 344
QY 355 VMESMTYLTAGMDQGFPPDCSIEAMVKVFSSEAAWQCSEALQILGGLGYTRDYPYER 414
DB 345 AARLLTYNAARLL-EAGKPFIK-EASMAKYASEIAGATTSCIEWMGVGYTKDYPVEK 402
QY 415 ILRDTTRILLIFEGTNEI 431
DB 403 YFRDAKIGTIYEGASNI 419

RESULT 12
US-09-252-991A-31097
; Sequence 31097, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31097
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31097

Query Match 19.1%; Score 603.5; DB 4; Length 419;
Best Local Similarity 38.7%; Pred. No. 2e-52;
Matches 136; Conservative 67; Mismatches 139; Indels 9; Gaps 6;
QY 88 DQEGKIPDETLEKLSGLGLFGLQVPEEYGGGLGFSNTMYS-RIGEISMDGSIITVTLAAHQ 146
DB 74 DREHFPAAEIREMADLGLGLMVLPEEWGGAQTGHAYAMALEEIAAGDAGACSTIMSVHN 133
QY 147 AIGLKGIIILAGTEQKAKYLPKLASGEHIAAECLETPASGSDASIRSRTLSEDKKHYI 206
DB 134 SVGCMPIHKFGSAEQERFLRPLAQGSLGALFALTEPQASDASFUKTRA--RRGDHYV 191
QY 207 LNSKVMITNGGLANIFTVPFAKTEVVDSDGSKVKDKITAFIVERDFGGVTKGPKEDKLGIR 266
DB 192 LNKAKQFITSQSHAGNVIFA---VTDPDAG-KRGISAFIVPTDTPGYEVVRIEDKLGQH 247
QY 267 GSNTCEVHFENTKIPVENILGEVGDGFKVAMNIIINSGRFSMGVSVAGLLKRLIEMTAEYA 326

Db 248 ASDTCQLAFNDLRIPATLRIGEGEYRIALANLEGGRIIAAQAQVMAAAFEAARDYA 307
QY 327 CTRKQFNRLSEFGLIOEKALMAQAQYVWESMTYLTAGMDQPGFPDSCIEAAMVKVFS 386
Db 308 HERETFGKPIEHOAVAFRLADNATRIAVARQMVH-HAASLREAGLP-CLTEASMAKLFA 365
QY 387 SEAAWQCVSEALQTLGLGVTYRDYPERILDRTRILLIFEGTNEILRMVIA 437
Db 366 SEMAEVCSAAITLGGYGLKDPFVERIYRDVRVCOIYEGTSDVQRLVIA 416
RESULT 13
US-09-328-352-6801
; Sequence 6801, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GPC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; EARLIER FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6801
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6801

Query Match 18.9%; Score 596; DB 4; Length 394;
Best Local Similarity 37.5%; Pred. No. 1e-51;
Matches 140; Conservative 73; Mismatches 138; Indels 22; Gaps 9;
QY 74 VEKFTTEVD--SRKIDQEGKIPEDELEKLSGLFGLQVPEYGGISNTMYSLGEI 131
Db 25 VAAFCABEIAPIAQVDQDNKFPFAHLWKFGDMGLLGMTVSEYGG---ANMGY--LAHI 79
QY 132 ISM-----DGSITVTLAAHOAIGLKIILAGTEEOKAKYLPKLASGEHIAAFCLEPAS 185
Db 80 IANQETISRAAATGLSVGAHNSLCVQINRNGEQKQKLPKLSGEYVGAAMSEPN 139
QY 186 GSDAASIRSRATLSDEKHHYLGSKVWITNGGLANFTVFAKTEVSDSGSVKDKITAF 245
Db 140 GSDVWSMKLRAEQKGD--HFVLNGSKWITNGGDADVLYVYAKT---DPQAGPKG-WTAF 193
QY 246 IVERDGGVTNGKPEDKLGIRGNTCEVHFNTKIPVENILGEVGDGFKVAMNLSGRF 305
Db 194 LIEKMGKFGSHGNDKLGMRGNTYPLFPFDNVEVPAENVLGGVNGVKVLSGLDYERA 253
QY 306 SMGSVAGLLKRLIEMTAECTRKQFNKRLSEFGLIOEKALMAQAQYVWESMTYLTAG 365
Db 254 VLSAGPLGINDACLDVVIPVILHOREFGQALGEFQLMQGLADNMYSTWLACKALVAVGA 313
QY 366 MLQDQFPDCSI--EAMVKVFSSEAAWQCVSEALQTLGLGVTYRDYPERILDRTRILL 423
Db 314 ACKADH-DRSLRKAASAILYAAEKATWAGEAIOITLGGYVINEFPFAGRLWRDAKLYE 372
QY 424 IFEGTNEILRMVYI 436
Db 373 IGAGTSEIRRMWLI 385

RESULT 14
US-09-364-230-30
; Sequence 30, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids

; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-364-230-30

Query Match 18.9%; Score 595.5; DB 3; Length 409;
Best Local Similarity 38.5%; Pred. No. 1.2e-51;
Matches 150; Conservative 64; Mismatches 143; Indels 33; Gaps 13;
QY 62 DELNEINQFLGVPKFFTEEV--DSRKIDQEGKIP--DETLEKLG-SLGLFGLQVPEYGG 117
Db 32 DTQGE--QFKSVHKEFAQETIAPHAAIDAASNHFFKDVNLKLMGDFNLHGLTAPEYGG 89
QY 118 LGFSNTMYS--RLGEIISMDGSITVTLAAHOAIGLKIILAGTEEOKAKYLPKLASGEHI 175
Db 90 MGL-GYMHCIAMEEINRASGSLSYSAHNSLNCINQLVRHGSQAOKLYLPKLITGEHV 148
QY 176 AAFCLTEPASGSDAASIRSRATLSDEKKH--YILNGSKVWITNGGLANFTVFAKTEV-V 232
Db 149 GALAMSEPNSSGSDVWSMKCA---EKYGGVINGNRKWCNGTNGSPSAQTLGVTAKTDTTA 204
QY 233 DSDGSKDKITAFIVERDGGVTNGKPEDKLGIRGNTCEVHFNTKIPVENILGEVGDG 292
Db 205 GSKG----ITAFIEKGMAGFSTAQKLDKLGMRGSDTCELVFENCFVPHENVLGEKG 259
QY 293 FKVAMNLSGRFSVAGLLKRLIEMTAECTRKQFNKRLSEFGLIOEKALMAQK 352
Db 260 VYVMSGLNLERFLAAGPSALMQACLDVAVLYVRQEQFGPIGEFQIRGKLADMYTS 319
QY 353 AVYVESMTYLT-----GMLDQPGPDCSI--EAMVKVFSSEAAWQCVSEALQTLGLGVT 407
Db 320 LOSSRSFVYSVARDCCNGKVDK---KDC-----AGVILFAAERATQVALQIOLGNGVYI 372
QY 408 RDPYVERILDRTRILLIFEGTNEILRMVIA 437
Db 373 NEYPTARLURDAKLFEGTSEIRRMIIA 402

RESULT 15
US-09-364-230-32
; Sequence 32, Application US/09364230
; Patent No. 6348339
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
; FILE REFERENCE: BB-1178
; CURRENT APPLICATION NUMBER: US/09/364,230
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,990
; EARLIER FILING DATE: July 31, 1998
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Glycine max
US-09-364-230-32

Query Match 18.7%; Score 588.5; DB 3; Length 427;
Best Local Similarity 37.6%; Pred. No. 6.9e-51;
Matches 143; Conservative 66; Mismatches 144; Indels 27; Gaps 10;

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OM protein - protein search, using sw model

Run on: April 25, 2005, 17:24:59 ; Search time 134 Seconds
(without alignments)
1542.263 Million cell updates/sec

Title: US-09-945-326-2
Perfect score: 3153
Sequence: 1 MSGCGLFRTTAAARACRGL.....SQILEKRAYICAHPLDRTC 621

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US10D_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3153	100.0	621	9 US-09-945-326-2	Sequence 2, Appli
2	3153	100.0	621	14 US-10-168-274-24	Sequence 24, Appl
3	3153	100.0	621	15 US-10-112-944-420	Sequence 420, App
4	3153	100.0	621	16 US-10-408-765A-1059	Sequence 1059, Ap
5	3153	100.0	621	16 US-10-408-765A-2053	Sequence 2053, Ap
6	3129	99.2	628	15 US-10-112-944-869	Sequence 869, App
7	1360	43.1	655	15 US-10-362-537-10	Sequence 10, Appl
8	1356.5	43.0	653	15 US-10-362-537-9	Sequence 9, Appli
9	1345	42.7	655	15 US-10-362-537-11	Sequence 11, Appl
10	1308	41.5	655	15 US-10-362-537-1	Sequence 1, Appli
11	1308	41.5	655	16 US-10-408-765A-534	Sequence 534, App
12	1299	41.2	655	16 US-10-408-765A-320	Sequence 320, App
13	1210.5	38.4	613	15 US-10-369-493-5444	Sequence 5444, Ap

14	954	30.3	188	16	US-10-408-765A-1442	Sequence 1442, Ap
15	954	30.3	188	16	US-10-408-765A-2052	Sequence 2052, Ap
16	844.5	26.8	594	15	US-10-369-493-16704	Sequence 16704, A
17	821	26.0	594	15	US-10-369-493-17429	Sequence 17429, A
18	816	25.9	581	15	US-10-369-493-19424	Sequence 19424, A
19	815.5	25.9	594	15	US-10-369-493-23285	Sequence 23285, A
20	798	25.3	585	15	US-10-369-493-9775	Sequence 9775, Ap
21	795.5	25.2	583	15	US-10-369-493-10383	Sequence 10383, A
22	765	24.3	583	15	US-10-369-493-16614	Sequence 16614, A
23	704	22.3	373	15	US-10-369-493-16614	Sequence 16614, A
24	699	22.2	382	15	US-10-369-493-16795	Sequence 16795, A
25	690	21.8	379	15	US-10-369-493-17460	Sequence 17460, A
26	686.5	21.8	377	15	US-10-369-493-9826	Sequence 9826, Ap
27	682	21.6	378	15	US-10-369-493-23196	Sequence 23196, A
28	678	21.5	381	15	US-10-369-493-16918	Sequence 16918, A
29	675.5	21.4	379	15	US-10-369-493-16613	Sequence 16613, A
30	659.5	20.9	646	14	US-10-156-761-10104	Sequence 10104, A
31	658	20.9	380	15	US-10-369-493-17459	Sequence 17459, A
32	652.5	20.7	379	15	US-10-369-493-23337	Sequence 23337, A
33	652	20.7	387	15	US-10-369-493-577	Sequence 577, App
34	644.5	20.6	384	14	US-10-272-419-6	Sequence 6, Appli
35	641	20.4	370	15	US-10-369-493-14087	Sequence 14087, A
36	640	20.3	375	15	US-10-369-493-8807	Sequence 8807, Ap
37	640	20.3	378	15	US-10-369-493-16449	Sequence 16449, A
38	633	20.1	375	15	US-10-369-493-17779	Sequence 17779, A
39	630.5	20.0	387	15	US-10-369-493-13698	Sequence 13698, A
40	629.5	20.0	381	15	US-10-369-493-546	Sequence 546, App
41	629	19.9	374	15	US-10-369-493-9830	Sequence 9830, Ap
42	626	19.9	373	15	US-10-369-493-11638	Sequence 11638, A
43	626	19.9	377	15	US-10-369-493-14685	Sequence 14685, A
44	625.5	19.8	379	15	US-10-369-493-10412	Sequence 10412, A
45	624	19.8	378	15	US-10-369-493-9086	Sequence 9086, Ap

ALIGNMENTS

RESULT 1

US-09-945-326-2
; Sequence 2, Application US/09945326
; Patent No. US20020127680A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Hunter, John Joseph
; TITLE OF INVENTION: 62112, A NOVEL HUMAN DEHYDROGENASE AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MNI-187
; CURRENT APPLICATION NUMBER: US/09/945,326
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,831
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-326-2

Query Match 100.0%; Score 3153; DB 9; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.7e-270;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGCGLFRTTAAARACRGLVSTANRRLLRTSPVRAFAKELFLGKIKKVEFPPEVS 60
DB 1 MSGCGLFRTTAAARACRGLVSTANRRLLRTSPVRAFAKELFLGKIKKVEFPPEVS 60
QY 61 QDELNEINFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFLGLQVPPEYGGGLGF 120
DB 61 QDELNEINFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFLGLQVPPEYGGGLGF 120
QY 121 SNTMYSRLGEIISMGDSITVTTLAAHQAIKGLIGLILAGTSEQAKYILPKUASGHIIAFLCL 180

Db 121 SNTWYRLGEIISMDGSIITVTLAAHQAIIGLGIILAGTEEQAKYLPKLASGEHIAAFCL 180
QY 181 TEPASGSDAASIESRATLSDDKHHYILNGSKWITNGGLANIFTVFAKTEVDSDGSVKD 240
Db 181 TEPASGSDAASIESRATLSDDKHHYILNGSKWITNGGLANIFTVFAKTEVDSDGSVKD 240
QY 241 KITAFIVERDFGVTNGKPEDKLGIKRSNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
Db 241 KITAFIVERDFGVTNGKPEDKLGIKRSNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
Db 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
QY 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILDRTR 420
Db 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILDRTR 420
QY 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDVD 480
Db 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDVD 480
QY 481 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
Db 481 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
QY 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
Db 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
QY 601 VSQQLKEKRAYICAHPLDRTC 621
Db 601 VSQQLKEKRAYICAHPLDRTC 621

RESULT 2

US-10-168-274-24
; Sequence 24, Application US/10168274
; Publication No. US20030124106A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: HILLMAN, Jennifer
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dying Aina M.
; TITLE OF INVENTION: HUMAN OXIDOREDUCTASE PROTEINS
; FILE REFERENCE: PF-0754 PCT
; CURRENT APPLICATION NUMBER: US/10/168,274
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/172,367
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124106A1 5540437CD1
US-10-168-274-24

Query Match 100.0%; Score 3153; DB 14; Length 621;

Best Local Similarity 100.0%; Pred. No. 2.7e-270;

Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGCGFLRTTAARACRGVAVSTANRLRTSPPVRAFAPAKELFLGKIKKKEVFPPEVPS 60
Db 1 MSGCGFLRTTAARACRGVAVSTANRLRTSPPVRAFAPAKELFLGKIKKKEVFPPEVPS 60

QY 61 QDELNEINQFLGVEKFFTEEVDSRKIDQEGKIPDETLEKLSLGLFGLQVPEYGGGLG 120
Db 61 QDELNEINQFLGVEKFFTEEVDSRKIDQEGKIPDETLEKLSLGLFGLQVPEYGGGLG 120
QY 121 SNTWYRLGEIISMDGSIITVTLAAHQAIIGLGIILAGTEEQAKYLPKLASGEHIAAFCL 180
Db 121 SNTWYRLGEIISMDGSIITVTLAAHQAIIGLGIILAGTEEQAKYLPKLASGEHIAAFCL 180
QY 181 TEPASGSDAASIESRATLSDDKHHYILNGSKWITNGGLANIFTVFAKTEVDSDGSVKD 240
Db 181 TEPASGSDAASIESRATLSDDKHHYILNGSKWITNGGLANIFTVFAKTEVDSDGSVKD 240
QY 241 KITAFIVERDFGVTNGKPEDKLGIKRSNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
Db 241 KITAFIVERDFGVTNGKPEDKLGIKRSNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
Db 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
QY 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILDRTR 420
Db 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILDRTR 420
QY 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDVD 480
Db 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDVD 480
QY 481 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
Db 481 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
QY 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
Db 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
QY 601 VSQQLKEKRAYICAHPLDRTC 621
Db 601 VSQQLKEKRAYICAHPLDRTC 621

RESULT 3

US-10-112-944-420
; Sequence 420, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 09/540,217
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: US 09/552,929
 ; PRIOR FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: US 09/577,408
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 924
 ; SOFTWARE: pt_FL_genes version 5.0
 ; SEQ ID NO 420
 ; LENGTH: 621
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-112-944-420

Query Match 100.0%; Score 3153; DB 15; Length 621;
 Best Local Similarity 100.0%; Pred. No. 2,7e-270;
 Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAPAKELFLGKIKKKEVFPPEVS 60
DB 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAPAKELFLGKIKKKEVFPPEVS 60
QY 61 QDELNEINQFLGPEVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLGQVPEEYGGIGF 120
DB 61 QDELNEINQFLGPEVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLGQVPEEYGGIGF 120
QY 121 SNTMYSLRGLIEIISMDGSIITVTLAAHQAIQGLKGIILAGTEEQAKYLPKLASGSHIAAFCL 180
DB 121 SNTMYSLRGLIEIISMDGSIITVTLAAHQAIQGLKGIILAGTEEQAKYLPKLASGSHIAAFCL 180
QY 181 TEPASGSDAASIRSRATLSEDKKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
DB 181 TEPASGSDAASIRSRATLSEDKKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
QY 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
DB 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
QY 301 NSGRFSGSVVAGLLKRLIEMTAETAEYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
DB 301 NSGRFSGSVVAGLLKRLIEMTAETAEYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
QY 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
DB 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
QY 421 ILLIFEGTNEILRMVYIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRITVD 480
DB 421 ILLIFEGTNEILRMVYIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRITVD 480
QY 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
DB 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
QY 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
DB 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
QY 601 VSQOILEKRAYICAHPLDRTC 621
DB 601 VSQOILEKRAYICAHPLDRTC 621
  
```

RESULT 4

US-10-408-765A-1059
 ; Sequence 1059, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1059
 ; LENGTH: 621
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-1059

Query Match 100.0%; Score 3153; DB 16; Length 621;
 Best Local Similarity 100.0%; Pred. No. 2,7e-270;
 Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAPAKELFLGKIKKKEVFPPEVS 60
DB 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAPAKELFLGKIKKKEVFPPEVS 60
QY 61 QDELNEINQFLGPEVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLGQVPEEYGGIGF 120
DB 61 QDELNEINQFLGPEVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLGQVPEEYGGIGF 120
QY 121 SNTMYSLRGLIEIISMDGSIITVTLAAHQAIQGLKGIILAGTEEQAKYLPKLASGSHIAAFCL 180
DB 121 SNTMYSLRGLIEIISMDGSIITVTLAAHQAIQGLKGIILAGTEEQAKYLPKLASGSHIAAFCL 180
QY 181 TEPASGSDAASIRSRATLSEDKKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
DB 181 TEPASGSDAASIRSRATLSEDKKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
QY 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
DB 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGFKVAMNII 300
QY 301 NSGRFSGSVVAGLLKRLIEMTAETAEYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
DB 301 NSGRFSGSVVAGLLKRLIEMTAETAEYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
QY 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
DB 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
QY 421 ILLIFEGTNEILRMVYIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRITVD 480
DB 421 ILLIFEGTNEILRMVYIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRITVD 480
QY 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
DB 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
QY 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
DB 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
QY 601 VSQOILEKRAYICAHPLDRTC 621
DB 601 VSQOILEKRAYICAHPLDRTC 621
  
```

RESULT 5

US-10-408-765A-2053
 ; Sequence 2053, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Wernock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2053
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-2053

Query Match 100.0%; Score 3153; DB 16; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.7e-270;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGCGFLRTTAAARACRGLVSTANRLLRTSPVPVAFKELFLGKIKKKEVFPPEVS 60
DB 1 MSGCGFLRTTAAARACRGLVSTANRLLRTSPVPVAFKELFLGKIKKKEVFPPEVS 60
QY 61 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 120
DB 61 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 120
QY 121 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEEQAKYLPKLASGEHIAAFCL 180
DB 121 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEEQAKYLPKLASGEHIAAFCL 180
QY 181 TEPASGDAASIRSRATLSDDKKHYILNGSKWITNGGLANITVFAKTEVVDSDGSVKD 240
DB 181 TEPASGDAASIRSRATLSDDKKHYILNGSKWITNGGLANITVFAKTEVVDSDGSVKD 240
QY 241 KITAFIVERDFGGVTNGKPDKLGIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
DB 241 KITAFIVERDFGGVTNGKPDKLGIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVWESMT 360
DB 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVWESMT 360
QY 361 YLTAGMLDQPGFPDSCIEAAWVKVFSSEAAWQCVSEALQILGLGYTRDYPYERILDRTR 420
DB 361 YLTAGMLDQPGFPDSCIEAAWVKVFSSEAAWQCVSEALQILGLGYTRDYPYERILDRTR 420
QY 421 ILLIFEGTNEILRMVIALTGLQHAGRIITRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480
DB 421 ILLIFEGTNEILRMVIALTGLQHAGRIITRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480
QY 481 LGITGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTTMESQLVKRVANILINL 540
DB 481 LGITGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTTMESQLVKRVANILINL 540
QY 541 YGMTAVLSRASRIRIGLRNHDHEVLLANTFCVEAYLQNLFSLSQLDKVPENLDSQIKK 600
DB 541 YGMTAVLSRASRIRIGLRNHDHEVLLANTFCVEAYLQNLFSLSQLDKVPENLDSQIKK 600
QY 601 VSQOILEKRAYICAHPLDRTC 621
DB 601 VSQOILEKRAYICAHPLDRTC 621

RESULT 6

US-10-112-944-869
; Sequence 869, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi

; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aicong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 869_
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(628)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fo
; OTHER INFORMATION: in Example 2
; US-10-112-944-869

Query Match 99.2%; Score 3129; DB 15; Length 628;
Best Local Similarity 99.2%; Pred. No. 3.7e-268;
Matches 616; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSGCGFLRTTAAARACRGLVSTANRLLRTSPVPVAFKELFLGKIKKKEVFPPEVS 60
DB 8 MSGCGFLRTTAAARACRGLVSTANRLLRTSPVPVAFKELFLGKIKKKEVFPPEVS 67
QY 61 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 120
DB 68 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 127
QY 121 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEEQAKYLPKLASGEHIAAFCL 180
DB 128 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEEQAKYLPKLASGEHIAAFCL 187
QY 181 TEPASGDAASIRSRATLSDDKKHYILNGSKWITNGGLANITVFAKTEVVDSDGSVKD 240
DB 188 TEPASGDAASIRSRATLSDDKKHYILNGSKWITNGGLANITVFAKTEVVDSDGSVKD 247
QY 241 KITAFIVERDFGGVTNGKPDKLGIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
DB 248 KITAFIVERDFGGVTNGKPDKLGIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 307
QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVWESMT 360
DB 308 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKPALMAQKAYVWESMT 367
QY 361 YLTAGMLDQPGFPDSCIEAAWVKVFSSEAAWQCVSEALQILGLGYTRDYPYERILDRTR 420

```
Db 368 YLTAGMLDQPGPDCIEAAWVKVFSSEAAWQCSEALQILGLGYTRDYPYERILDR 427
QY 421 ILLIFGTNEILMYIALTGLQHAGRIILTRIHELKQAKVSTYMDTVGRRRLRSLGR 480
Db 428 ILLIFGTNEILMYIALTGLQHAGRIILTRIHELKQAKVSTYMDTVGRRRLRSLGR 487
QY 481 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETILIRFGKTIIMEQVLKRVANIL 540
Db 488 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETILIRFGKTIIMEQVLKRVANIL 547
QY 541 YGTAIVLSRASIRIRIGLRNHDHVEILLANTFCVEAYLQNLFSLSQLDKYPENLD 600
Db 548 YGTAIVLSRASIRIRIGLRNHDHVEILLANTFCVEAYLQNLFSLSQLDKYPENLD 607
QY 601 VSQIILEKRAYICAHPLDRTC 621
Db 608 VSQIILEKRAYICAHPLDRTC 628

RESULT 7
US-10-362-537-10
; Sequence 10, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Mouse
US-10-362-537-10

* Query Match
Best Local Similarity 43.1%; Score 1360; DB 15; Length 655;
Matches 287; Conservative 106; Mismatches 184; Indels 18; Gaps 9;

QY 35 PVRA-----FAKELFLGKIKKKEVFPPEV-SODELNEINQFLGPVEKFFTEEVDSRKIDQ 89
Db 66 PARAEKSKFAVGMFKGQLTIDQVFPVPSVLSBEQAQFLKELGVPARFEEVNDPAKND 125
QY 90 EKKIPDETLEKLSLGLFGLGVPEEYGGFGFNTMYSRLGEIISM-DGSITVTTLAAHQAI 148
Db 126 LEKVEDDTLQGLKELGAFGLQVPSLGLGLSNTQYARLAEIVGMHDLGVSVTLGAHQSI 185
QY 149 GLKGITLAGEOKAKVLPKLASGEHIAAFLTEPASGSDAASIRSATLSSEDKKHYYLN 208
Db 186 GFKGILLYGTAKQREKYLPRVAGQALAAFLTEPSSGSDVASIRSAIPSPCGKYTYLN 245
QY 209 GSKVWITNGLANIFTVFAKTEVVD-SDGSVKDKITAFIVERDFGVNGKPEDKLGIRG 267
Db 246 GSKIWLSNGGLADIFTVFAKTPKDAATGAVKEKITAFAVVERSGVTHGLPEKMGKGA 305
QY 268 SNTCEVHPENTKIPVENILGEVGDGPKVAMNLSGRFSVGSVAGLLKRLIEMTAEYAC 327
Db 306 SNTSEVYFDGVKVPSENVLGEVGDGPKVAVNLLNNGRFGMAATLAGTMRKSLIAKAVDHAT 365
QY 328 TRKQFNKRLSEGLIOEKALMAQKAYMESMTYLTAGMLDQPGPDCIEAAWVKVFS 387
Db 366 NRTQFGDKIHNFVIOEKRLAMAILQYVTESMAYMLSANNDQ-GPKDFQIEAAISKIPCS 424
QY 388 EAAWQCSEALQILGLGYTRDYPYERILDRTRILLIFEGTNEILMYIALTGLQHAGRI 447
Db 425 EAAKWVADCEIQLMGGMGFMKPEGVVERVLRDIRIFRIFEGANDILRLFVALQCMKDGKE 484
QY 448 LTRIHELKQ--AKVSTVMDTVGRRRLRSLGRITVDLGLTGNHGVVHPSLADSANKFEENT 505
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```
Db 485 LTGLGNALKNPFGNVGLMGEAGKQRRRTGIGSGLSLS---GIVHPELSRSGELAVQAL 541
QY 506 YCFGRVTETILIRFGKTIIMEEQVLKRVANILNYGMTAVLSRASIRIRIGLRNHDHEV 565
Db 542 DQFATVVEAKLVKHKGIQVNEQFLQLADGALDLYAMVVVLSRASRSLSEGYPYTAQHEK 601
QY 566 LIANTFCVRA---YLQNLFSLSQLDKYPENLDQIKKVSQQILEKRAYICAHPL 617
Db 602 MLCDSWCIEAATRIRENMASSQSPQH--QELFRNFRSISKAMVENGGLVTGNPL 654

RESULT 8
US-10-362-537-9
; Sequence 9, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Rat
US-10-362-537-9

Query Match
Best Local Similarity 43.0%; Score 1356.5; DB 15; Length 653;
Matches 295; Conservative 108; Mismatches 192; Indels 41; Gaps 12;

QY 9 RTTAAARACRGLVSVSTANRRLLR-----TSPPVRA-----FAKELFLGKIKKKEV 53
Db 32 RPTSAQR---LVASEATQAVLEKPELTSSDASTREKPARAEKSKFAVGMFKGQLTIDQV 87
QY 54 FPPPEVSQDELANE-----INQFLGPVEKFFTEEVDSRKIDQEGKIPEDETLEKLSLGLFG 108
Db 88 FPPPSV---LNEGQTQFLKELGVPARFEEVNDPAKNDLSLEKVEEDTLQGLKELGAFG 143
QY 109 LQVPEYGGFGFNTMYSRLGEIISM-DGSITVTTLAAHQAIQGLKGIILAGTEEQKAKYLP 167
Db 144 LQVPSLGLGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGPKGILLYGTAKQEKYLP 203
QY 168 KLASGEHIAAFLTEPASGSDAASIRSATLSSEDKKHYYLNGSKVWITNGGLANIETVFA 227
Db 204 RVASGQALAAFLCTEPSSGSDVASIRSSAVSPSPCGKYTYLNGSKIWSNGGLADIFTVFA 263
QY 228 KTEVVD-SDGSVKDKITAFIVERDFGVNGKPEDKLGIRGSGNTCEVHPENTKIPVENIL 286
Db 264 KTIKDAATGAVKEKITAFAVVERSGVTHGLPEKMGKIKASNTSEVYFDGVKVPANVL 323
QY 287 GSVGDGPKVAMNLSGRFSVGSVAGLLKRLIEMTAEYACTRKQFNKRLSEGLIOEK 346
Db 324 GEVGDGPKVAVNLLNNGRFGMAATLAGTMRKSLIAKAVDHATNRTQFGDKIHNFVIOEKL 383
QY 347 ALMAQKAYMESMTYLTAGMLDQPGPDCIEAAWVKVFSSEAAWQCSEALQILGLGY 406
Db 384 ARMAILQYVTESMAYMLSANNDQ-GPKDFQIEAAISKIPGSEAAWVTDCEIQLMGGMGF 442
QY 407 TRDYPYERILDRTRILLIFEGTNEILMYIALTGLQHAGRIILTRIHELKQ--AKVSTVM 464
Db 443 MKEPGVERVLRDIRIFRIFEGTNDILRLFVALQCMKDGKELTGLGNALKNPGLNVLGLLI 502
QY 465 DTVGRRLRSLGRITVDLGLTGNHGVVHPSLADSANKFEENTYCFGTETILLRFGKTI 524
Db 503 GEASKQLRRTTIGSGLSLS---GIVHPELSRSGELAVQALBOFATVVEAKLMMKKHGIV 559
```

```
QY 525 EEQVLVKRVANILNLYGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEA---YLQNLF 581
Db 560 NEQFLQLRLADCAIDLAMVVLVLRASRSISEGPTAQHEKMLCDSWCIEAATIRENMA 619
QY 582 SLSQLDKYAPENLDEQIKKVSQQILEKRAYICAHPL 617
Db 620 SLSQNPQ--QQELPRNFRSISKAMVENGGLVTSNPL 653

RESULT 9
US-10-362-537-11
; Sequence 11, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Bovine
US-10-362-537-11

Query Match 42.7%; Score 1345; DB 15; Length 655;
Best Local Similarity 47.3%; Pred. No. 5,8e-110;
Matches 285; Conservative 110; Mismatches 194; Indels 14; Gaps 9;

QY 23 STANRRLLRTPPPAPAKELFGIKKKEVFPPEV-SODELNEINQFLGPVKEPFTTEE 81
Db 57 SEASTREKRANSVSKSPAVGTFKQLTTDQVFPYPSVLNEDQTFKLKELVGPVTRFEEV 116
QY 82 VDSRKIDQCKIPDETLEKLSLGLFGLQVPEYGGVGFNTMYSLRGLHISM-DGSITV 140
Db 117 NDAKNDMLSERVETMQGKELGAGFGLQVPELGGVGLCNTQYARLVEIVGMDLGVGI 176
QY 141 TLAHQAGLGLGKILAGTEQKAKYLPKLASGHEHIAAFCLTEPASGSDAASIRSRATLSE 200
Db 177 VLGAHQSIGFKGILLFCTKAQKYLPLKASGETIAAFCLTEPSSGSDAASIRSAVSP 236
QY 201 DKHYILNGSKWITNGGLANIITVFAKTEVVD--SDGSVKDKITAFIVERDFGVTNGKP 259
Db 237 CGKYITLNGSKIWISNGGLADIITVFAKTEVTDATGAVKEKITAFVVERSGGVTHGPP 296
QY 260 EDKLGIRGNTCEVHPENTKIPVENILGEVGDGFKVAMNLSGRFSMGSVVGAGLKRLI 319
Db 297 EKGWIKASNTAEVDFGVVRPAENVLGEVGGFKVAMHLLNNGRFGMAALAGTWKGI 356
QY 320 EMTAEYACTRKQFNKRLSEFGLIQERFALMAQKAYMESMTYLTAGMLDQGPFPDCSIEA 379
Db 357 AKAVDHAANTQFGKIHNFGLIQELARWMLQYVTESMAYMVSAAMDQ-GSTDFQIERA 415
QY 380 AMKVFSSEAAWQCSEALQILGGLGYTRDYPYERILDRTRILLIPEGTNEILRMVIALT 439
Db 416 AISKIFGSEAAWQTECQIMGMGMFKPEPGVERVRLDRIFRIFEGTNDILRLFVALQ 475
QY 440 GLQHAGRLITRIHELKQ--AKVSTVMDTVGRRLRDSLGRTVDLGTGNHGVVHPSLADS 497
Db 476 GCMWDKGLSGLGNALKNPFGNAGLLGEAGKQLRRRAGLSGLS---GIVHQELSR 532
QY 498 ANKFEENTYCFGRVETLLRFGKTIMEQVLKRVANILNLYGMTAVLSRASRSIRIG 557
Db 533 GELAVQALEQFATVWAKLHKHKKDIINEQFLQLRLADSAIDLAMVVLVLRASRSISLSE 592
QY 558 LRNHDHVEVLANTFCVEA---YLQNLFSLSQLDKYAPENLDEQIKKVSQQILEKRAYICA 614
Db 593 HPTAQHEKMLCDSWCIEAARIENMTAL-QSDPQQOE-LFRNFKSISKALVERGGVTS 650
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QY 615 HPL 617
Db 651 NPL 653
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RESULT 10
US-10-362-537-1
; Sequence 1, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 1
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Human
US-10-362-537-1
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Query Match 41.5%; Score 1308; DB 15; Length 655;
Best Local Similarity 46.9%; Pred. No. 1.1e-106;
Matches 276; Conservative 106; Mismatches 194; Indels 12; Gaps 8;

QY 37 RAPAKELFLGKIKKKEVFPPEV-SODELNE-INQFLGPVKEPFTTEVDSRKIDQCKIPD 95
Db 71 KSFVGMFGKQLTTDQVFPYPSVLNEDQTFKLKELVGPVTRFEEVNDPAKNDALMEVSE 130
QY 96 ETLEKLSLGLFGLQVPEYGGVGFNTMYSLRGLHISM-DGSITVTLAAHQAGLGLKII 154
Db 131 TTWQGLKELGAGFGLQVPSLGGVGLCNTQYARLVEIVGMDLGVGITLGAHQSIGFKGIL 190
QY 155 LAGTEQKAKYLPKLASGHEHIAAFCLTEPASGSDAASIRSRATLSEDKHYILNGSKWI 214
Db 191 LFGTKAQKELPLKASGETVAAAFCLTEPSSGSDAASIRTSAPSPCGKYITLNGSKLWI 250
QY 215 TNGGLANIITVFAKTEVVD--SDGSVKDKITAFIVERDFGVTNGKPEDKLGIRGNTCEV 273
Db 251 SNGGLADIITVFAKTEVTDATGAVKEKITAFVVERSGGITHGPEKKWGIKASNTAEV 310
QY 274 HPENTKIPVENILGEVGDGFKVAMNLSGRFSMGSVVGAGLKRLIEMTAETACTRKQFN 333
Db 311 PFDGVVRPSENVLGEVSGFKVAMHLLNNGRFGMAALAGTWKGIITAKAVDHAATNRQFG 370
QY 334 KRLSEFGLIQERFALMAQKAYMESMTYLTAGMLDQGPFPDCSIEAMVKVFSSEAAWQC 393
Db 371 EKIHNFGLIQELARWMLQYVTESMAYMVSAAMDQ-GATDFQIEAAISKIFGSEAAWKV 429
QY 394 VSEALQILGGLGYTRDYPYERILDRTRILLIPEGTNEILRMVIALTGLQHAGRLITRIH 453
Db 430 TDECQIMGMGMFKPEPGVERVRLDRIFRIFEGTNDILRLFVALQCMCKKELSGLS 489
QY 454 ELKQ--AKVSTVMDTVGRRLRDSLGRTVDLGTGNHGVVHPSLADSANKFEENTYCFGR 511
Db 490 ALKNPFGNAGLLGEAGKQLRRRAGLSGLS---GLVHPELSRSGELAVRALQFATV 546
QY 512 VETLLRFGKTIMEQVLKRVANILNLYGMTAVLSRASRSIRIGLRNHDHVEVLANTFF 571
Db 547 VBAKLIKHKHKKDIINEQFLQLRLADCAIDLAMVVLVLRASRSISLSEGHPTAQHEKMLCDTW 606
QY 572 CYE--AYLQNLFSLSQLDKYAPENLDEQIKKVSQQILEKRAYICAHPL 617
Db 607 CIEAARIREGMAALQSDPQQOE-LYRNFKSISKALVERGGVTSNPL 653
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RESULT 11

Db	61	LADSANKFEENTYCFGRVTETLLRFGKTIMEEQVLKRVANILINLYGMTAVLSRSRS	120
Qy	554	IRIGLENDHDEVLANTFCVEAYLQNLFSLSQDKYAPENLDBQIKKVSQQILEKRAYIC	613
Db	121	IRIGLENDHDEVLANTFCVEAYLQNLFSLSQDKYAPENLDBQIKKVSQQILEKRAYIC	180
Qy	614	AHPLDRTC	621
Db	181	AHPLDRTC	188

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Job time : 136 secs

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